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Reviewer: markspencer

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Application No: 10591040 Version No: 1.0

Input Set:

Output Set:

Started: 2007-07-09 15:49:13.986
Finished: 2007-07-09 15:49:14.335
Elapsed: 0 hr(s) 0 min(s) 0 sec(s) 349 ms
Total Warnings: 2
Total Errors: 0
No. of SeqIDs Defined: 2
Actual SeqID Count: 2

Error code	Error Description
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SEQUENCE LISTING

<110> F. Hoffmann-La Roche AG

<120> Method for the purification of an N-terminal fragment of
hepatocyte growth factor

<130> 22389 WO

<140> 10591040

<141> 2007-07-09

<150> EP 04004950.4

<151> 2004-03-03

<160> 2

<170> PatentIn version 3.2

<210> 1

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<212> DNA

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<223> dna coding for NK4

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aag act acc cta atc aaa ata gat cca gca ctg aag ata aaa acc aaa	96
Lys Thr Thr Leu Ile Lys Ile Asp Pro Ala Leu Lys Ile Lys Thr Lys	
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aaa gtg aat act gca gac caa tgt gct aat aga tgt act agg aat aaa	144
Lys Val Asn Thr Ala Asp Gln Cys Ala Asn Arg Cys Thr Arg Asn Lys	
35 40 45	

gga ctt cca ttc act tgc aag gct ttt gtt ttt gat aaa gca aga aaa	192
Gly Leu Pro Phe Thr Cys Lys Ala Phe Val Phe Asp Lys Ala Arg Lys	
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caa tgc ctc tgg ttc ccc ttc aat agc atg tca agt gga gtg aaa aaa	240
Gln Cys Leu Trp Phe Pro Phe Asn Ser Met Ser Ser Gly Val Lys Lys	
65 70 75 80	

gaa ttt ggc cat gaa ttt gac ctc tat gaa aac aaa gac tac att aga	288
Glu Phe Gly His Glu Phe Asp Leu Tyr Glu Asn Lys Asp Tyr Ile Arg	
85 90 95	

aac tgc atc att ggt aaa gga cgc agc tac aag gga aca gta tct atc	336
Asn Cys Ile Ile Gly Lys Gly Arg Ser Tyr Lys Gly Thr Val Ser Ile	
100 105 110	
act aag agt ggc atc aaa tgt cag ccc tgg agt tcc atg ata cca cac	384
Thr Lys Ser Gly Ile Lys Cys Gln Pro Trp Ser Ser Met Ile Pro His	
115 120 125	
gaa cac agc ttt ttg cct tcg agc tat cgg ggt aaa gac cta cag gaa	432
Glu His Ser Phe Leu Pro Ser Ser Tyr Arg Gly Lys Asp Leu Gln Glu	
130 135 140	
aac tac tgt cga aat cct cga ggg gaa gaa ggg gga ccc tgg tgt ttc	480
Asn Tyr Cys Arg Asn Pro Arg Gly Glu Glu Gly Gly Pro Trp Cys Phe	
145 150 155 160	
aca agc aat cca gag gta cgc tac gaa gtc tgt gac att cct cag tgt	528
Thr Ser Asn Pro Glu Val Arg Tyr Glu Val Cys Asp Ile Pro Gln Cys	
165 170 175	
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Ser Glu Val Glu Cys Met Thr Cys Asn Gly Glu Ser Tyr Arg Gly Leu	
180 185 190	
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Met Asp His Thr Glu Ser Gly Lys Ile Cys Gln Arg Trp Asp His Gln	
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Thr Pro His Arg His Lys Phe Leu Pro Glu Arg Tyr Pro Asp Lys Gly	
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tgc tat act ctt gac cct cac acc cgc tgg gag tac tgt gca att aaa	768
Cys Tyr Thr Leu Asp Pro His Thr Arg Trp Glu Tyr Cys Ala Ile Lys	
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Tyr Met Gly Asn Leu Ser Gln Thr Arg Ser Gly Leu Thr Cys Ser Met
370 375 380

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Trp Asp Lys Asn Met Glu Asp Leu His Arg His Ile Phe Trp Glu Pro
385 390 395 400

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405 410 415

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taa tag 1350

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Gly Leu Pro Phe Thr Cys Lys Ala Phe Val Phe Asp Lys Ala Arg Lys

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His Glu His Asp Met Thr Pro Glu Asn Phe Lys Cys Lys Asp Leu Arg
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Glu Asn Tyr Cys Arg Asn Pro Asp Gly Ser Glu Ser Pro Trp Cys Phe
325 330 335

Thr Thr Asp Pro Asn Ile Arg Val Gly Tyr Cys Ser Gln Ile Pro Asn
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Cys Asp Met Ser His Gly Gln Asp Cys Tyr Arg Gly Asn Gly Lys Asn
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Tyr Met Gly Asn Leu Ser Gln Thr Arg Ser Gly Leu Thr Cys Ser Met
370 375 380

Trp Asp Lys Asn Met Glu Asp Leu His Arg His Ile Phe Trp Glu Pro
385 390 395 400

Asp Ala Ser Lys Leu Asn Glu Asn Tyr Cys Arg Asn Pro Asp Asp Asp
405 410 415

Ala His Gly Pro Trp Cys Tyr Thr Gly Asn Pro Leu Ile Pro Trp Asp
420 425 430

Tyr Cys Pro Ile Ser Arg Cys Glu Gly Asp Thr Thr Pro Thr Ile Val
435 440 445